

MAR 1 9 7003



1600

TECH CENTER 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/276,935D

TIME: 15:11:09

DATE: 03/13/2003

4	<110>	APPLICANT: KLIEWER, Steven A.	
5		JONES, Stacey A.	
6		WILLSON, Timothy M.	
		TITLE OF INVENTION: AN ORPHAN NUCLEAR RECEPTOR	
		FILE REFERENCE: PU3474US2	
13	<140>	CURRENT APPLICATION NUMBER: 09/276,935D	
		CURRENT FILING DATE: 2002-11-27	
16	<150>	PRIOR APPLICATION NUMBER: 60/079,593	
17	<151>	PRIOR FILING DATE: 1998-03-27	
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		ORGANISM: Artificial Sequence	
		FEATURE:	
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		SEQUENCE: 3	
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		LENGTH: 31	
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		ORGANISM: Artificial Sequence	
		FEATURE:	
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RAW SEQUENCE LISTING

DATE: 03/13/2003 PATENT APPLICATION: US/09/276,935D TIME: 15:11:09

67 <210> SEQ JD NO: 5	
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128 <223> OTHER INFORMATION: Probe	
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/276,935D TIME: 15:11:09

DATE: 03/13/2003

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141 <223> OTHER INFORMATION: His6-PXR Fusion Protein
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146 Thr Gln Pro Leu Gly Val Gln Gly Leu Thr Glu Glu Gln Arg Met Met
147 20
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148 Ile Arg Glu Leu Met Asp Ala Gln Met Lys Thr Phe Asp Thr Thr Phe
150 Ser His Phe Lys Asn Phe Arg Leu Pro Gly Val Leu Ser Ser Gly Cys
                        55
152 Glu Leu Pro Glu Ser Leu Gln Ala Pro Ser Arg Glu Glu Ala Ala Lys
                     70
154 Trp Ser Gln Val Arg Lys Asp Leu Cys Ser Leu Lys Val Ser Leu Gln
                 85
156 Leu Arg Gly Glu Asp Gly Ser Val Trp Asn Tyr Lys Pro Pro Ala Asp
157 100
                               105
158 Ser Gly Gly Lys Glu Ile Phe Ser Leu Leu Pro His Met Ala Asp Met
159 115 120
                                    125
160 Ser Thr Tyr Met Phe Lys Gly Ile Ile Ser Phe Ala Lys Val Ile Ser
161 130 135 140
162 Tyr Phe Arg Asp Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu Lys Gly
                     150
                                       155
164 Ala Ala Phe Glu Leu Cys Gln Leu Arg Phe Asn Thr Val Phe Asn Ala
                                    170
166 Glu Thr Gly Thr Trp Glu Cys Gly Arg Leu Ser Tyr Cys Leu Glu Asp
                               185
167 180
168 Thr Ala Gly Gly Phe Gln Gln Leu Leu Glu Pro Met Leu Lys Phe
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170 His Tyr Met Leu Lys Lys Leu Gln Leu His Glu Glu Glu Tyr Val Leu
                        215
172 Met Gln Ala Ile Ser Leu Phe Ser Pro Asp Arg Pro Gly Val Leu Gln
                    230
                                      235
174 His Arg Val Val Asp Gln Leu Gln Glu Gln Phe Ala Ile Thr Leu Lys
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                                   250
176 Ser Tyr Ile Glu Cys Asn Arg Pro Gln Pro Ala His Arg Phe Leu Phe
             260 265
178 Leu Lys Ile Met Ala Met Leu Thr Glu Leu Arg Ser Ile Asn Ala Gln
179 275
                            280
180 His Thr Gln Arg Leu Leu Arg Ile Gln Asp Ile His Pro Phe Ala Thr
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182 Pro Leu Met Gln Glu Leu Phe Gly Ile Thr Gly Ser
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183 305
186 <210> SEQ ID NO: 12
187 <211> LENGTH: 242
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' RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/276,935D TIME: 15:11:09

DATE: 03/13/2003

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189 <213> ORGANISM: Artificial Sequence
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192 <223> OTHER INFORMATION: RXR Alpha Proten
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                                    25
199 Asn Met Gly Leu Asn Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile
                                40
201 Cys Gln Ala Ala Asp Lys Gln Lou Phe Thr Leu Val Glu Trp Ala Lys
                            55
203 Arg Ile Pro His Phe Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu
                                            75
204 65
                        70
205 Leu Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg
                                        90
207 Ser Ile Ala Val Lys Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val
               100
                                    105
209 His Arg Asn Ser Ala His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg
210
           115
                                120
211 Val Leu Thr Glu Leu Val Ser Lys Met Arg Asp Met Gln Met Asp Lys
                            135
212 130
                                                140
213 Thr Glu Leu Gly Cys Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser
                       150
                                           155
215 Lys Gly Leu Ser Asn Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val
                                        170
                    165
217 Tyr Ala Ser Leu Glu Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro
218
                180
                                    185
219 Gly Arg Phe Ala Lys Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile
          195
220
                                200
                                                    205
221 Gly Leu Lys Cys Leu Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp
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223 Thr Pro Ile Asp Thr Phe Leu Met Glu Met Leu Glu Ala Pro His Gln
224 225
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225 Met Thr
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235 <223> OTHER INFORMATION: Probe
237 <400> SEQUENCE: 13
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239 gacgggaaga ggaagcactg cetttactte agtgggaate teggeeteag cetgeaagee 120
240 aagtgttcac agtgagaaaa gcaagagaat aagctaatac teetgteetg aacaaggcag 180
241 eggeteettg gtaaagetae teettgateg ateetttgea eeggattgtt caaagtggae 240
242 cccaggggag aagtcggagc aaagaactta ccaccaagca gtccaagagg cccagaagca 300
243 aacctggagg tgagacccaa agaaagctgg aaccatgctg actttgtaca ctgtgaggac 360
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RAW SEQUENCE LISTING

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245 atctgccgtg tatgtgggga caaggccact ggctatcact tcaatgtcat gacatgtgaa 480
246 ggatgcaagg gctttttcag gagggccatg aaacgcaacg cccggctgag gtgccccttc 540
247 eggaagggeg cetgegagat caceeggaag acceggegae agtgeeagge etgeegeetg 600
248 cgcaagtgcc tggagagcgg catgaagaag gagatgatca tgtccgacga ggccgtggag 660
249 gagaggcggg cettgateaa geggaagaaa agtgaaegga eagggaetea geeaetggga 720
250 gtgcaggggc tgacagagga gcagcggatg atgatcaggg agctgatgga cgctcagatg 780
251 aaaacctttg acactacctt cteecatttc aagaatttee ggetgeeagg ggtgettage 840
252 agtqqctqcq aqttqccaqa qtctctqcaq qccccatcqa qqqaaqaaqc tqccaaqtqq 900
253 agecaggice ggaaagatet gigetetitig aaggietete igeagetigeg gggggaggat 960
254 ggcagtgtct ggaactacaa acccccagcc gacagtggcg ggaaagagat cttctccctg 1020
255 etgececaca tggetgacat gteaacetae atgtteaaag geateateag etttgecaaa 1080
256 gteateteet aetteaggga ettgeeeate gaggaeeaga teteeetget gaagggggee 1140
257 gctttcgagc tgtgtcaact gagattcaac acagtgttca acgeggagac tggaacctgg 1200
258 gagtgtggcc ggctgtccta ctgcttggaa gacactgcag gtggcttcca gcaacttcta 1260
259 ctggagccca tgctgaaatt ccactacatg ctgaagaagc tgcagctgca tgaggaggag 1320
260 tatgtgctga tgcaggccat ctccctcttc tccccagacc gcccaggtgt gctgcagcac 1380
261 cgcgtggtgg accagctgca ggagcaattc gccattactc tgaagtccta cattgaatgc 1440
262 aatoggcccc agoctgctca taggttcttg ttcctgaaga tcatggctat gctcaccgag 1500
263 cteegeagea teaatgetea geacacceag eggetgetge geateeagga catacaccee 1560
264 tttgctacgc ccctcatgca ggagttgttc ggcatcacag gtagctgagc ggctgccctt 1620
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268 tcagtctgta gggagtgaag ccacagactc ttacgtggag agtgcactga cctgtaggtc 1860
269 aggaccatca gagaggcaag gttgcccttt ccttttaaaa ggccctgtgg tctggggaga 1920
270 aatccctcag atcccactaa agtgtcaagg tgtggaaggg accaagcgac caaggatagg 1980
271 ccatctgggg tctatgccca catacceacg tttgttcgct tcctgagtct tttcattgct 2040
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273 tgggetecag geetgtacte ateggeaggt geatgagtat etgtgg
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276 <211> LENGTH: 434
277 <212> TYPE: PRT
278 <213> ORGANISM: Homo Sapien
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286 Glu Glu Val Gly Gly Pro Gln Ile Cys Arg Val Cys Gly Asp Lys Ala
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288 Thr Gly Tyr His Phe Asn Val Met Thr Cys Glu Gly Cys Lys Gly Phe
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290 Phe Arg Arg Ala Met Lys Arg Asn Ala Arg Leu Arg Cys Pro Phe Arg
291 65
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292 Lys Gly Ala Cys Glu Ile Thr Arg Lys Thr Arg Arg Gln Cys Gln Ala
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294 Cys Arg Leu Arg Lys Cys Leu Glu Ser Gly Met Lys Lys Glu Met Ile
295
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VERIFICATION SUMMARY

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TIME: 15:11:10